

Comprehensive grid search is used to determine the possible range for the two parameters in the Michaelis-Menten equation. After evaluating the model with many combinations of parameters, the nonlinear regression estimated the best fitting reduction rate as a formula of mercury concentration to be:

$$r = 9.957 * [CH_3Hg^+] / (2.78 + [CH_3Hg^+])$$

With high statistical significance under 95% confidence interval.

Although the parameter values differed from the Philippidis values of 17.5 nmol of Hg/min/mg protein and 3.6  $\mu$ M, respectively. Our fitted equation was on a similar order of magnitude and the differences from the Philippidis values may result from different experimental methods and the difference between methylmercury and ionic mercury conversion behavior.

Our fitted equation exhibited difference from the experimental data possible because methylmercury is poisonous to *E.coli* above certain concentration threshold. Thus, our experimental data at higher methylmercury concentration is limited by *E.coli* cell death and the Michaelis Menten equation used does not account for cell death. For specifics on the fit of the formula, refer to

**Supplemental Materials B.**